

CAG ATG GAT CCT AAT AGA ATA TCA GAA GAT GGC ACT CAC TGC ATT TAT Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr 1 5 10 15	48
AGA ATT TTG AGA CTC CAT GAA AAT GCA GAT TTT CAA GAC ACA ACT CTG Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu 20 25 30	96
GAG AGT CAA GAT ACA AAA TTA ATA CCT GAT TCA TGT AGG AGA ATT AAA Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys 35 40 45	144
CAG GCC TTT CAA GGA GCT GTG CAA AAG GAA TTA CAA CAT ATC GTT GGA Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly 50 55 60	192
TCA CAG CAC ATC AGA GCA GAG AAA GCG ATG GTG GAT GGC TCA TGG TTA Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu 65 70 75 80	240
GAT CTG GCC AAG AGG AGC AAG CTT GAA GCT CAG CCT TTT GCT CAT CTC Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu 85 90 95	288
ACT ATT AAT GCC ACC GAC ATC CCA TCT GGT TCC CAT AAA GTG AGT CTG Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu 100 105 110	336
TCC TCT TGG TAC CAT GAT CGG GGG TGG GGT AAG ATC TCC AAC ATG ACT Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr 115 120 125	384
TTT AGC AAT GGA AAA CTA ATA GTT AAT CAG GAT GGC TTT TAT TAC CTG Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu 130 135 140	432
TAT GCC AAC ATT TGC TTT CGA CAT CAT GAA ACT TCA GGA GAC CTA GCT Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala 145 150 155 160	480
ACA GAG TAT CTT CAA CTA ATG GTG TAC GTC ACT AAA ACC AGC ATC AAA Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys 165 170 175	528
ATC CCA AGT TCT CAT ACC CTG ATG AAA GGA GGA AGC ACC AAG TAT TGG Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp 180 185 190	576
TCA GGG AAT TCT GAA TTC CAT TTT TAT TCC ATA AAC GTT GGT GGA TTT Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe 195 200 205	624
TTT AAG TTA CGG TCT GGA GAG GAA ATC AGC ATC GAG GTC TCC AAC CCC Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro 210 215 220	672
TCC TTA CTG GAT CCG GAT CAG GAT GCA ACA TAC TTT GGG GCT TTT AAA Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys 225 230 235 240	720

Figure 1

GTT CGA GAT ATA GAT TGA G C C C C A G T T T T T G G A G T G T T A T G T A T T T C C	768
Val Arg Asp Ile Asp *	
245	
TGGATGTTTG GAAACATTTT TTAAACAAG CCAAGAAAGA TGTATATAGG TGTGTGAGAC	828
TACTAAGAGG CATGGCCCAA CGGTACACGA CTCAGTATCC ATGCTCTTGA CCTGTAGAG	888
AACACGCGTA TTTACAGCCA GTGGGAGATG TTAGACTCAT GGTGTGTTAC ACAATGGTTT	948
TTAAATTTTG TAATGAATTC CTAGAATTAA ACCAGATTGG AGCAATTACG GGTGACCTT	1008
ATGAGAACT GCATGTGGGC TATGGGAGGG GTTGGTCCCT GGTATGTGC CCCTTCGCAG	1068
CTGAAGTGA GAGGGTGTCA TCTAGCGCAA TTGAAGGATC ATCTGAAGGG GCAAATCTT	1128
TTGAATGTT ACATCATGCT GGAACCTGCA AAAAATACTT TTTCTAATGA GGAGAGAAAA	1188
TATATGATT TTTATATAAT ATCTAAAGTT ATATTCAGA TGTAAATGTT TCTTGCAAA	1248
GTTATGTAAA TTATATTTGT GCTATAGTAT TTGATCAAA ATATTTAAAA ATGTCTTGCT	1308
GTTGACATAT TTAATGTTTT AAATGTACAG ACATATTTAA CTGGTGCACT TTGTAAATTC	1368
CCTGGGGAAA ACTTGCAGCT AAGGAGGGGA AAAAATGTTG TTTCTAATA TCAAATGCAG	1428
TATATTTCTT CGTTCTTTTT AAGTTAATAG ATTTTTCAG ACTTGTCAAG CCTGTGCAAA	1488
AAAAATAAAA TGGATGCCTT GAATAATAAG CAGGATGTTG GCCACCAGGT GCCTTTCAAA	1548
TTTAGAACT AATTGACTTT AGAAAGCTGA CATTGCCAAA AAGGATACAT AATGGGCCAC	1608
TGAAATCTGT CAAGAGTAGT TATATAATTG TTGAACAGGT GTTTTCCAC AAGTGCCGCA	1668
AATTGTACCT TTTTTGTTT TTTTCAAAAT AGAAAAGTTA TTAGTGGTTT ATCAGCAAAA	1728
AAGTCCAATT TTAATTTAGT AAATGTTATC TTATACTGTA CAATAAAAAC ATTGCCTTTG	1788
AATGTAAAT TTTTGGTACA AAAGTCGACG GCCGC	1823

Figure 1 (continued)

Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Gly Thr His Cys Ile Tyr
 1 5 10 15
 Arg Ile Leu Arg Leu His Glu Asn Ala Asp Phe Gln Asp Thr Thr Leu
 20 25 30
 Glu Ser Gln Asp Thr Lys Leu Ile Pro Asp Ser Cys Arg Arg Ile Lys
 35 40 45
 Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
 50 55 60
 Ser Gln His Ile Arg Ala Glu Lys Ala Met Val Asp Gly Ser Trp Leu
 65 70 75 80
 Asp Leu Ala Lys Arg Ser Lys Leu Glu Ala Gln Pro Phe Ala His Leu
 85 90 95
 Thr Ile Asn Ala Thr Asp Ile Pro Ser Gly Ser His Lys Val Ser Leu
 100 105 110
 Ser Ser Trp Tyr His Asp Arg Gly Trp Gly Lys Ile Ser Asn Met Thr
 115 120 125
 Phe Ser Asn Gly Lys Leu Ile Val Asn Gln Asp Gly Phe Tyr Tyr Leu
 130 135 140
 Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Asp Leu Ala
 145 150 155 160
 Thr Glu Tyr Leu Gln Leu Met Val Tyr Val Thr Lys Thr Ser Ile Lys
 165 170 175
 Ile Pro Ser Ser His Thr Leu Met Lys Gly Gly Ser Thr Lys Tyr Trp
 180 185 190
 Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
 195 200 205
 Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser Ile Glu Val Ser Asn Pro
 210 215 220
 Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys
 225 230 235 240
 Val Arg Asp Ile Asp *
 245

Figure 2

CCCACGTC CC GGGGAGCCAC TGCCAGGACC TTTGTGAACC GGTGCGGGCG GGGGCCGTGG	60
CGGAGTCTGC TCGGCGGTGG GTGGCCCGAG AAGGGAGAGA ACGATCGCGG AGCAGGGCGC	120
CCGAACTCCG GCGGCCGCGC C ATG CGC CGG GCC AGC CGA GAC TAC GGC AAG	171
Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys	250 255
TAC CTG CGC AGC TCG GAA GAG ATG GGC AGC GGC CCC GGC GTC CCA CAC	219
Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro Gly Val Pro His	260 265 270
GAA GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT CCG GCG CCG CCA	267
Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro	275 280 285
CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG GGG CTG GGA CTG	315
Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Gly Leu Gly Leu	290 295 300
GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC TTT CGA GCG CAG	363
Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln	305 310 315 320
ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC TGC TTT TAT AGA	411
Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg	325 330 335
ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC TCG ACT CTG GAG	459
Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu	340 345 350
AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG AAA CAA GCC TTT	507
Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe	355 360 365
CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG GGG CCA CAG CGC	555
Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg	370 375 380
TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG TTG GAT GTG GCC	603
Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala	385 390 395 400
CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC CTC ACC ATC AAT	651
Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn	405 410 415
GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT CTG TCC TCT TGG	699
Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp	420 425 430
TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG ACG TTA AGC AAC	747
Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn	435 440 445
GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC CTG TAC GCC AAC	795
Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn	450 455 460
ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA CCT ACA GAC TAT	843
Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr	465 470 475 480

Figure 3

CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC AAA ATC CCA AGT Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser 485 490 495	891
TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC TGG TCG GGC AAT Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn 500 505 510	939
TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA TTT TTC AAG CTC Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu 515 520 525	987
CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC CCT TCC CTG CTG Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu 530 535 540	1035
GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC AAA GTT CAG GAC Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp 545 550 555 560	1083
ATA GAC TGA GACTCATTTT GTGGAACATT AGCATGGATG TCCTAGATGT Ile Asp *	1132
TTGGAAACTT CTAAAAAAT GGATGATGTC TATACATGTG TAAGACTACT AAGAGACATG	1192
GCCCCACGGTG TATGAAACTC ACAGCCCTCT CTCTTGAGCC CTGTACAGGT TGTGTATATG	1252
TAAAGTCCAT AGGTGATGTT AGATTCATGG TGATTACACA ACGGTTTAC AATTTTGTA	1312
TGATTTCTTA GAATTGAACC AGATTGGGAG AGGTATTCGG ATGCTTATGA AAAACTTACA	1372
CGTGAGCTAT GGAAGGGGGT CACAGTCTCT GGTCTAACCC CTGGACATGT GCCACTGAGA	1432
ACCTTGAAAT TAAGAGGATG CCATGTCATT GCATAGAAAT GATAGTGTGA AGGGTTAAGT	1492
TCTTTTGAAT TGTTACATTG CGCTGGGACC TGCAAATAAG TTCTTTTTTT CTAATGAGGA	1552
GAAAAATATA TGTATTTTTA TATAATGTCT AAAGTTATAT TTCAGGTGTA ATGTTTCTG	1612
TGCAAAGTTT TGTAATTAT ATTTGTGCTA TAGTATTTGA TTCAAAATAT TTAAAAATGT	1672
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GCAAAATAAA TAAATAAAAA TAAATGAAT ACCTTGAATA ATAAGTAGGA TGTTGGTCAC	1912
CAGGTGCCTT TCAAATTTAG AAGCTAATTG ACTTTAGGAG CTGACATAGC CAAAAAGGAA	1972
CATAATAGGC TACTGAAATC TGTCAGGAGT ATTTATGCAA TTATTGAACA GGTGTCTTTT	2032
TTTACAAGAG CTACAAATTG TAAATTTTGG TTTCTTTTTT TTCCCATAGA AAATGTACTA	2092
TAGTTTATCA GCCAAAAAC AATCCACTTT TTAATTTAGT GAAAGTTATT TTATTATACT	2152
GTACAATAAA AGCATTGTCT CTGAATGTTA ATTTTTTGGT ACAAAAAATA AATTGTACG	2212
AAAAAAAAA AAAAAAAAAA AAAAA	2237

Figure 3 (continued)

Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
 1 5 10 15
 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
 20 25 30
 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Ala Ala Ser Arg Ser
 35 40 45
 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
 50 55 60
 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
 65 70 75 80
 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
 85 90 95
 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
 100 105 110
 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
 115 120 125
 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
 130 135 140
 Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
 145 150 155 160
 Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
 165 170 175
 Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
 180 185 190
 Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
 195 200 205
 Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
 210 215 220
 Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
 225 230 235 240
 Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
 245 250 255
 Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
 260 265 270
 Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
 275 280 285
 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
 290 295 300
 Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp *
 305 310 315

Figure 4

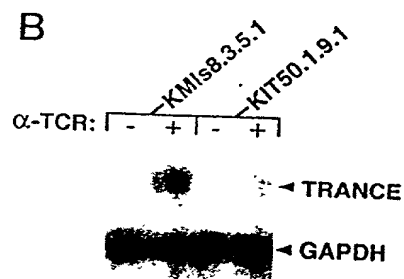
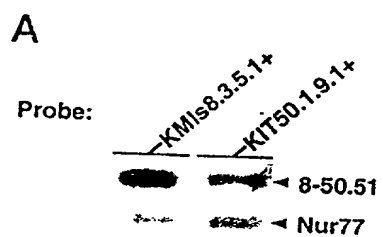


Figure 5

A

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1  MPRASRDYGYK*LRSSRMGSGGVPHEGFLHPAPAPAPAPPAPASRSMFIALGLGLGO mTRACE
61  VVCSIALFLYFRAQMDPNRISEDSTHCYFPLRLUEHAGIQDSTLESDT--LPDSCFRM mTRACE
      .....G.....I.....DF..T....Q..KL.....I hTRACE
119 KQAFQGAQAVQKELQHIVGQRQRFSGAPAMMEGSLWDVAORKGKPEAQFFAHLTINAASIPSGS mTRACE
      .....S.HIRAEM.VD.....L.K.S.L.....TD..... hTRACE
179 HKVTLSSWYHDRGWAKISNMTLSNGKLRRVNQDGFYLYLANICFRHHETSGSVPTDYLQLM mTRACE
      .....S.....G.....F.....I.....DLA.E..... hTRACE
239 VVVVKTSIKIPSSINLMKGSSTKNWSGNSEFIHFYSINVGGFFKLRAGEEISIQVNSPSLL mTRACE
      .....T.....T.....Y.....S.....E..... hTRACE
249 DPDDOATYFGAFYVDVID 315 mTRACE
      .....R..... hTRACE

```

B

120 AAKGAVTPECHIVGQRFEGAPAEIEGSGWVQVQAEAPQPSLILIA----- mTRACE
101 DPH-----PSPPEITDLSLYSFEKATANTSPKERS----- mFasL
87 IYI-----IEELTITDPTITIP-----EASTPLNLRGPQV----- mTRAIL
93 HPQRSNAGRMSTSQGVACRSRSKMTIISFADSTFECQOLPKSEETDLNPE mLT-Beta
60 -----RDEKELGLPLILSKYITPLSSQNSSITPLVVAHQ----- mTNF-alpha

B C D

172 ---MPSGSHKVT---PCHD-RGWKISNNTLS---KPEPPEELANIC--- mTRACE
152 -----HSRSIP---EIDTY---GTALISVYKKK---ILEA--- mFasL
142 I-PLKTKT-LIKIEEPEKNGHSNHLVFR---EIEIETIIEE mTRAIL
153 LPAPHLILAWMSQVLEAALVE-EAPRPAQFSPTHALPQVMLLCHQVYR mLT-Beta
101 -----VEEQ---EELTGA-MPLAMMDLKDN-QAPAPALGGLK mTNF-alpha

E F

225 TSGS-----VPTDYVQVAVVYTIKIRHNINCKSTN-----WSGN--- mTRACE
199 G-----NDQITNIP---MRRNSK---EDLILNINILYITGQI--- mFasL
198 AEDARKMVGK---EERH---VITYS---DPPHLSA---LSGS---RDAYGL mTRAIL
211 TLAG---RSRPSRSALALAGAG---GPPEPILAEATVTVVNTVYGL--- mLT-Beta
147 G-----LTLHTS---FAI---QEKVNLASAVK-SPEKDTLEALKKPE mTNF-alpha

G H I

273 QVMVEK---PEELIQVQVHP---EDTVMSGL---ODID mTRACE
240 GPKASNNITGALYV---HQLIN---EESKSNLYL mFasL
251 LQCYEKKKNIISITELHML---EESKSNLYL mTRAIL
266 VGFALA---SVYV---HMLY-PPKMLVVMVG mLT-Beta
195 P---EKKQAEINLY---AESQVYVIAL mTNF-alpha

Figure 6

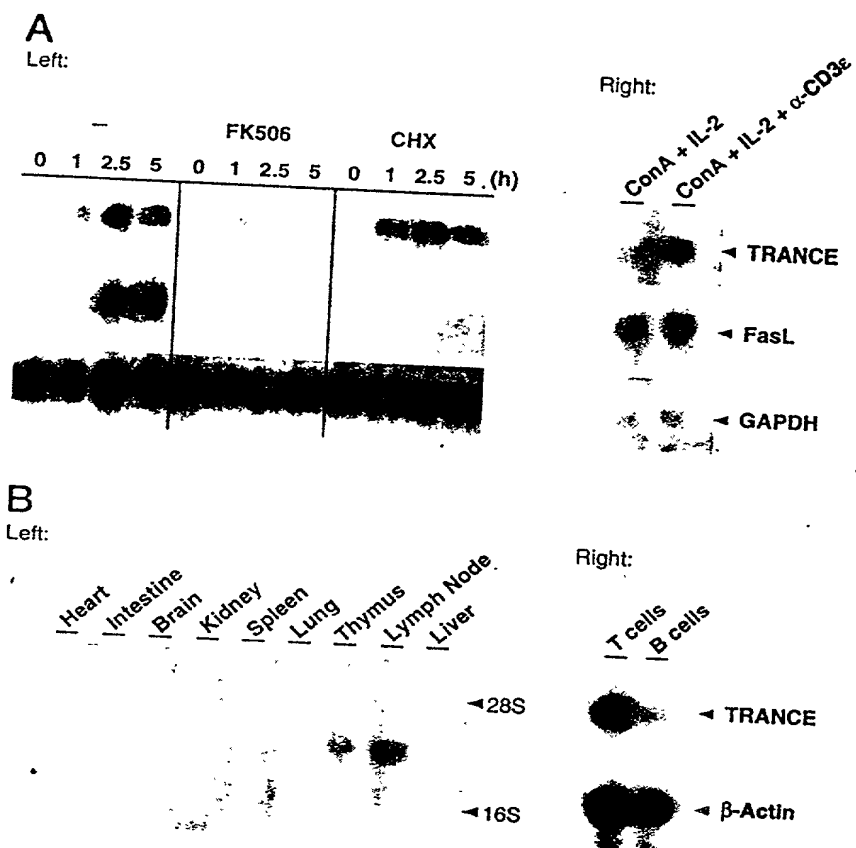


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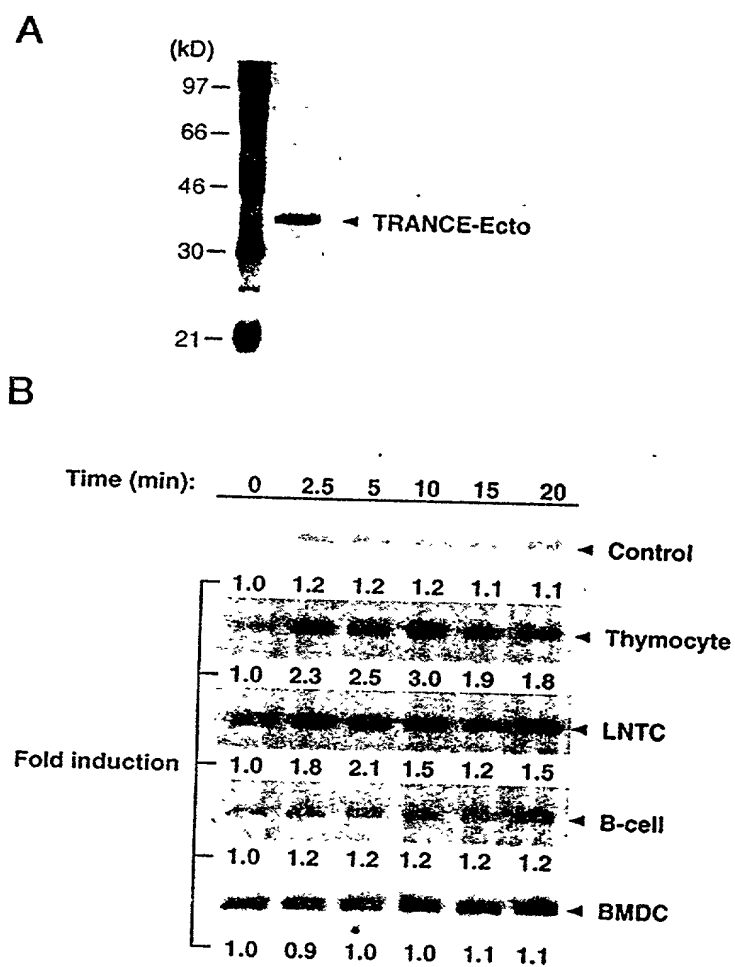


Figure 8

600-1-200M CIP

(Sheet 11 of 26)

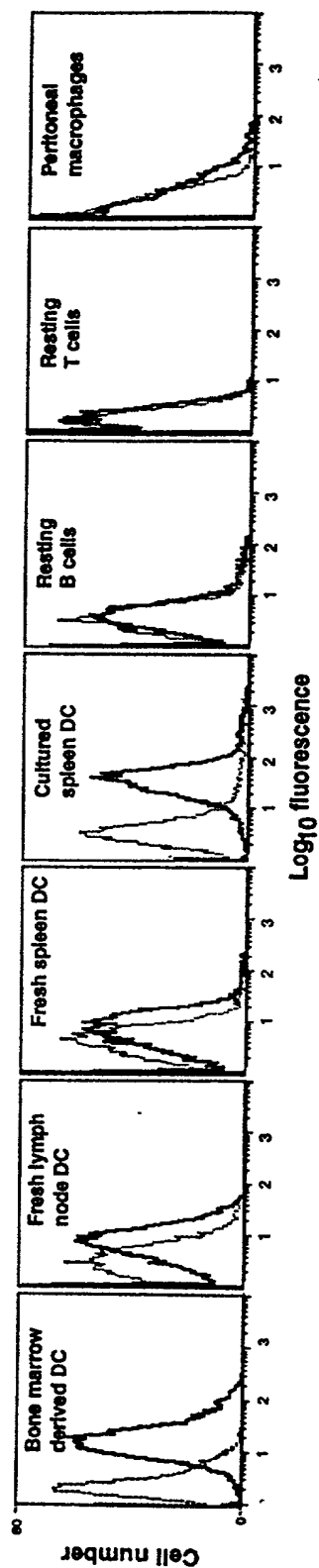


Figure 9

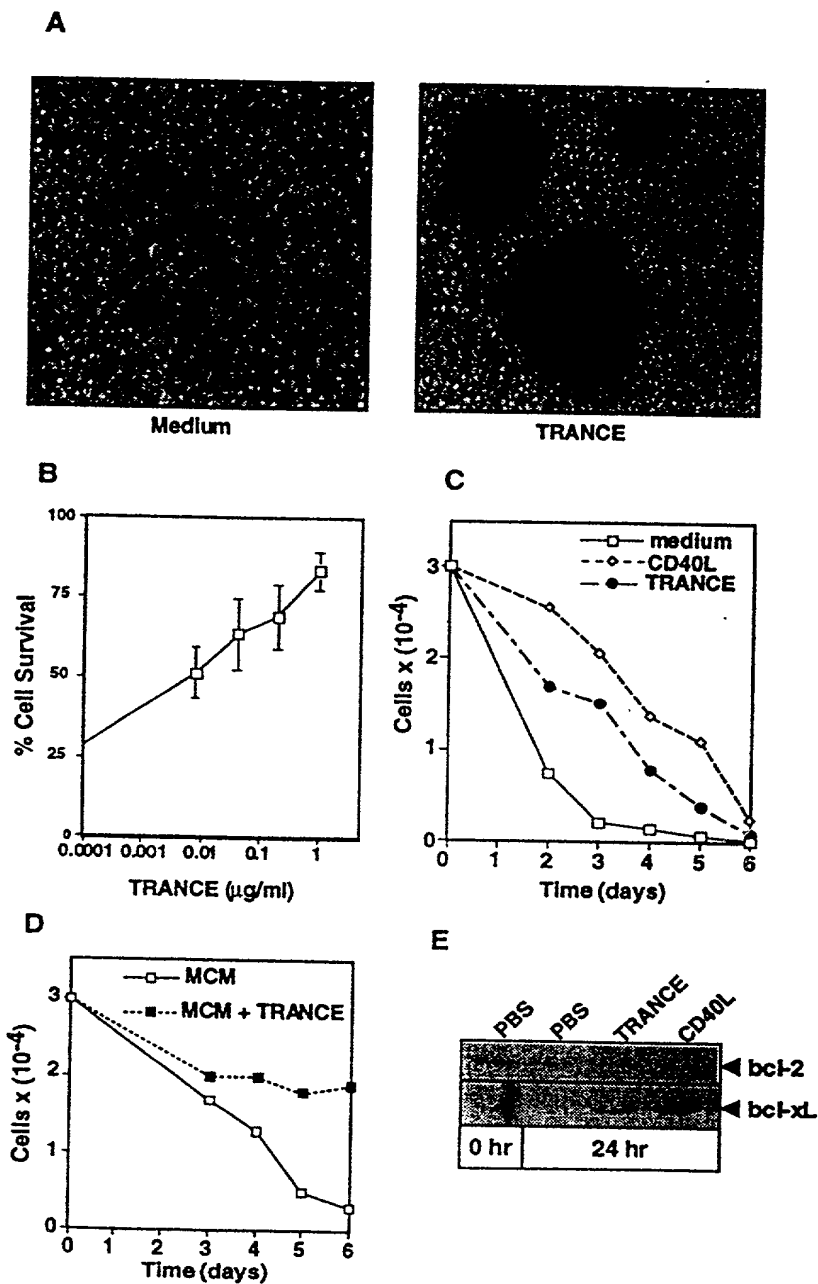


Figure 10

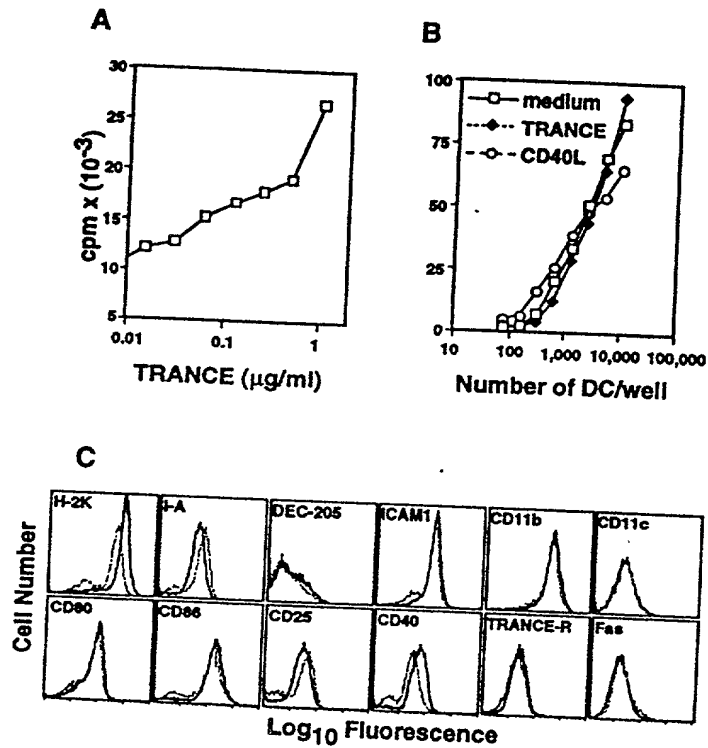


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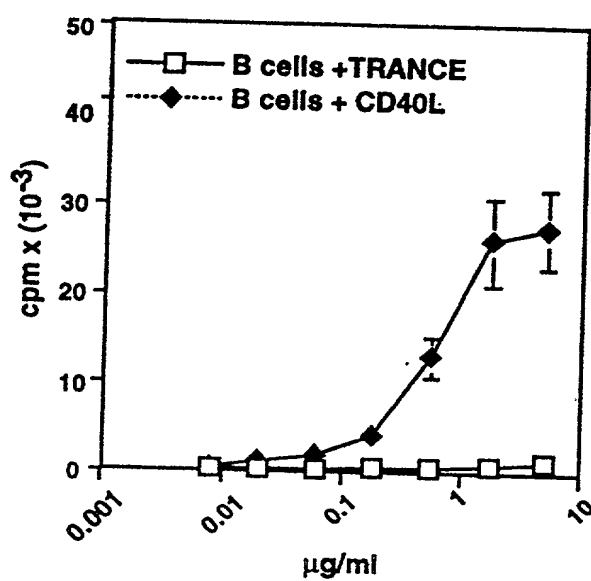


Figure 12

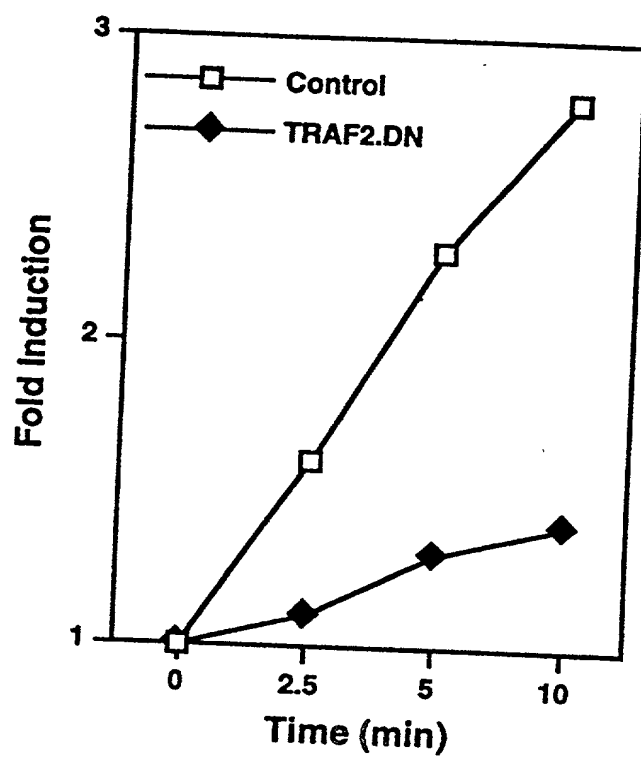


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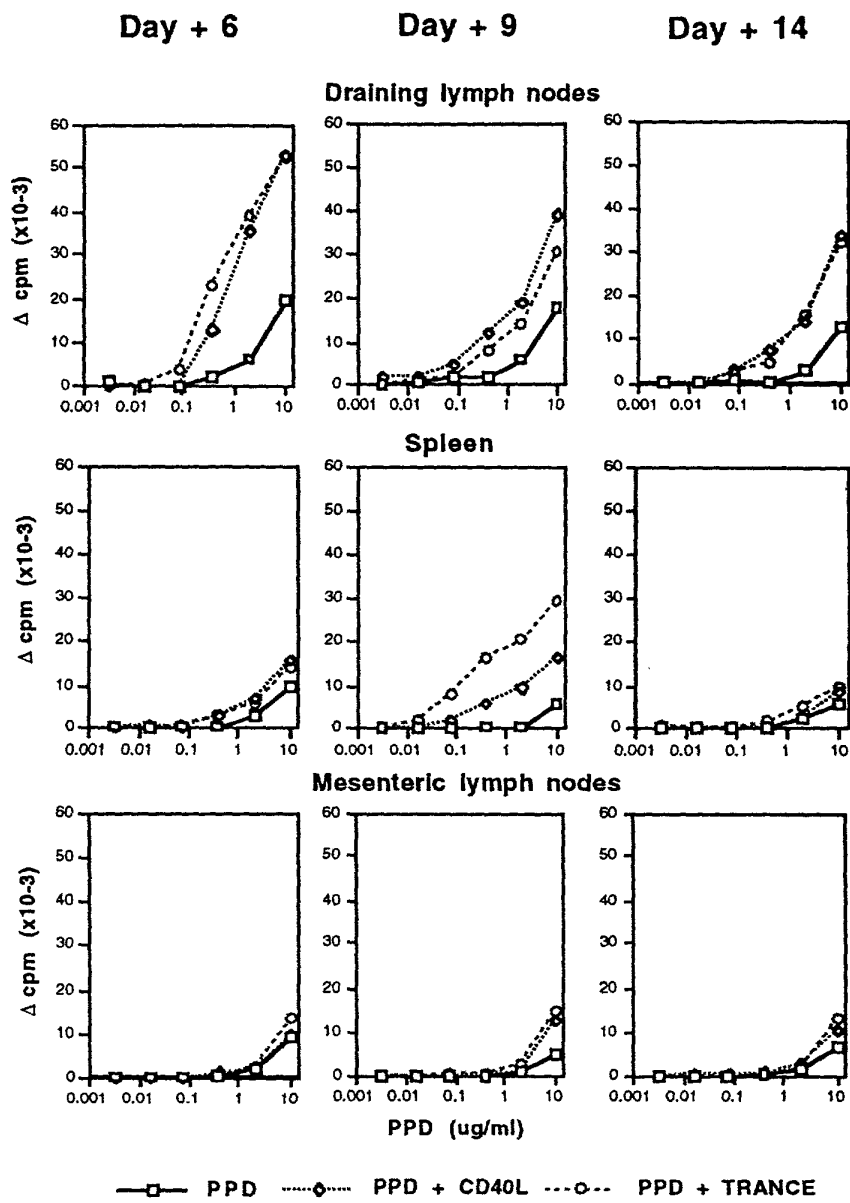


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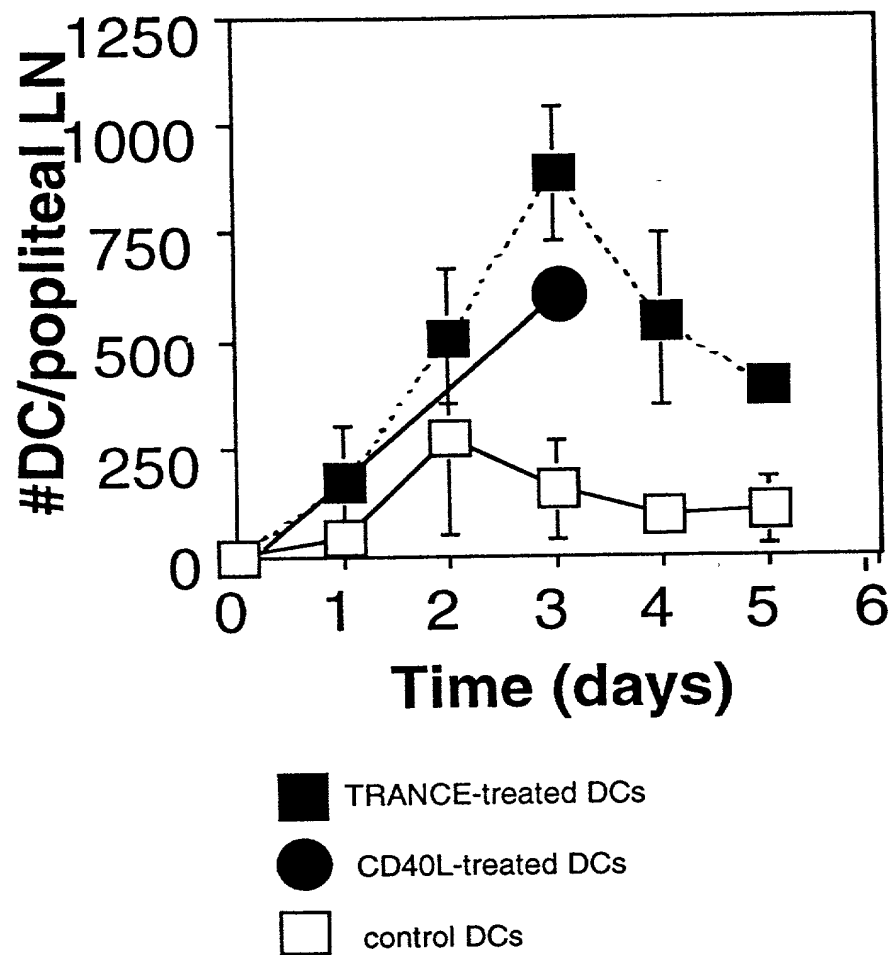


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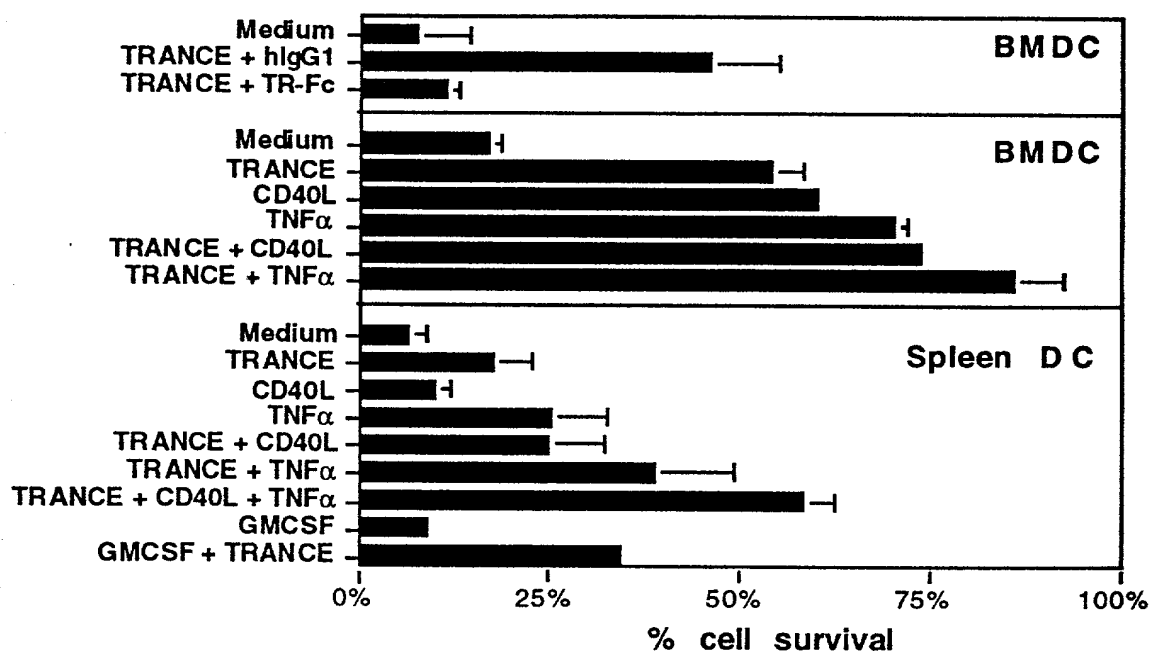


Figure 16

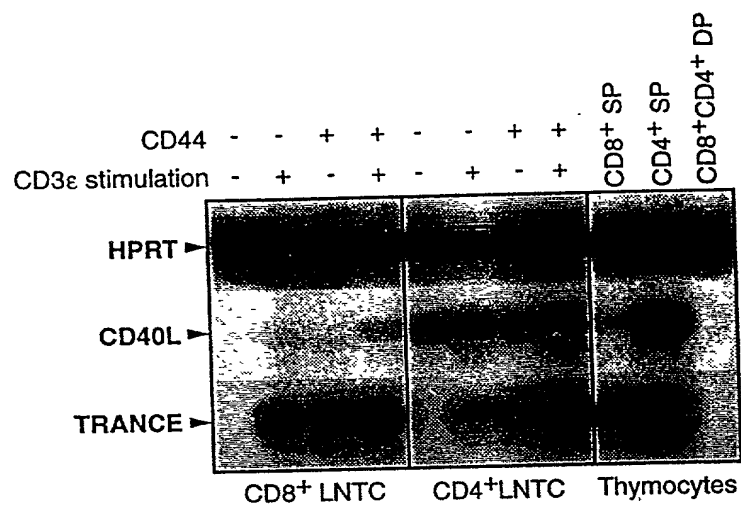


Figure 17

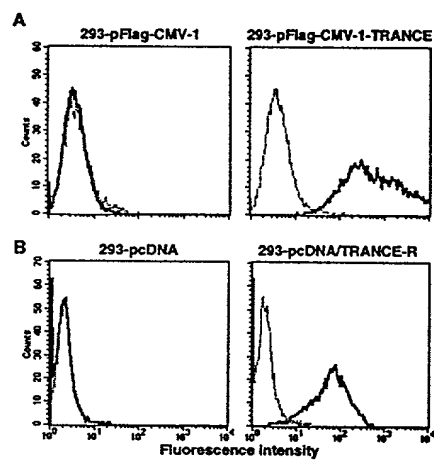


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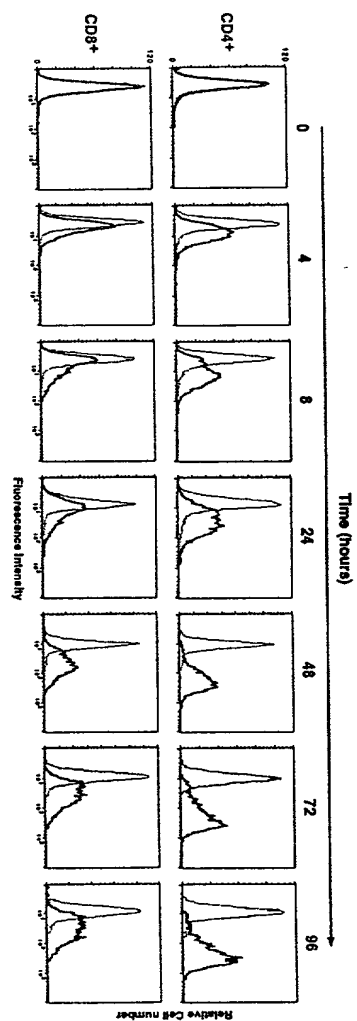


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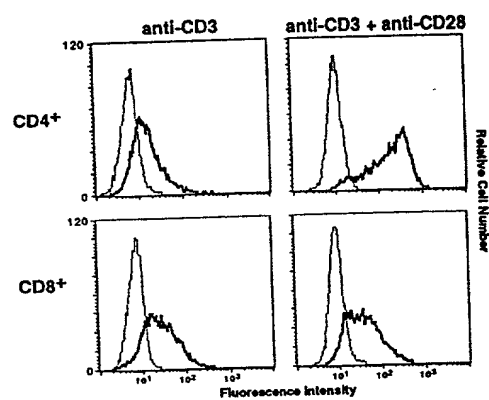


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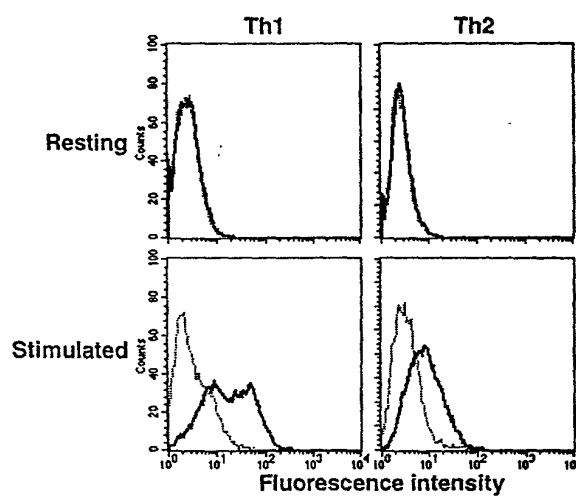


Figure 21

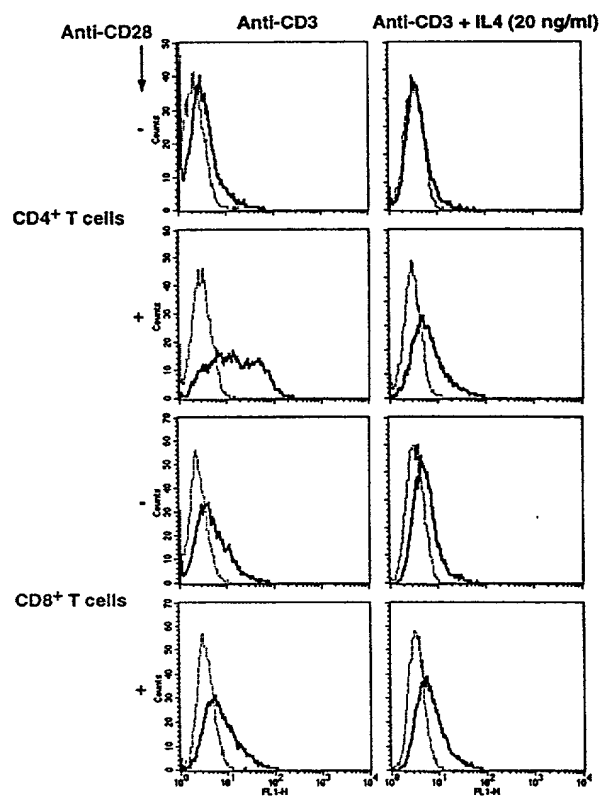


Figure 22

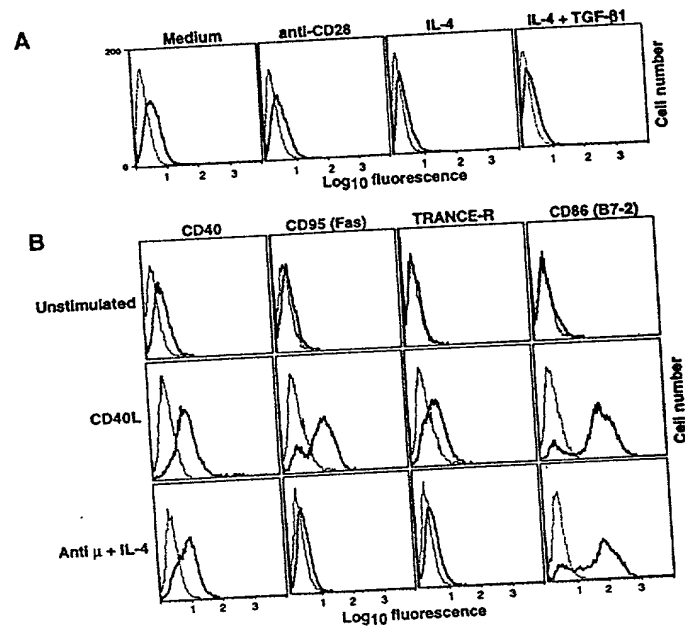


Figure 23

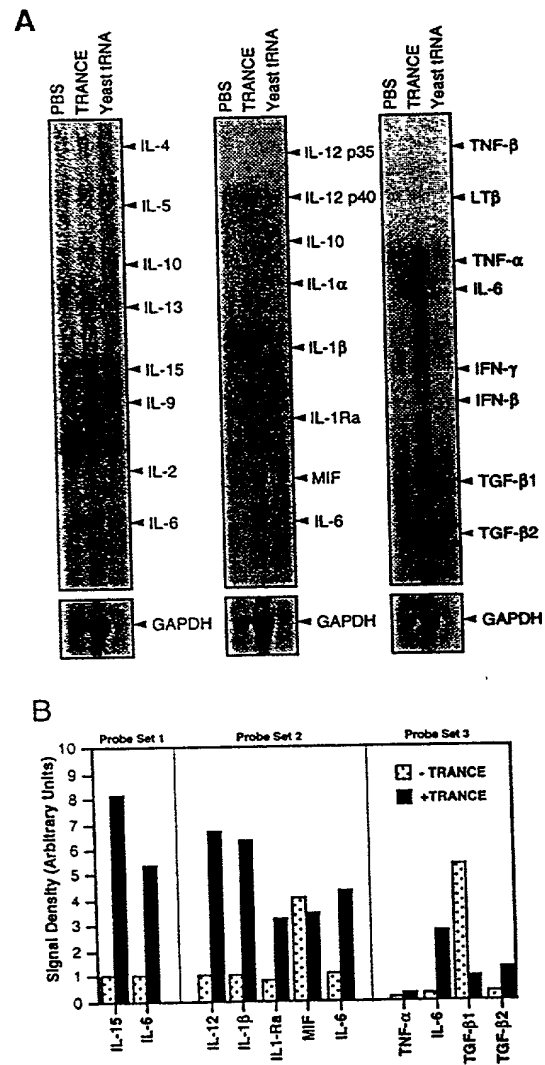


Figure 24